

SEQUENCE LISTING

<110> University of Rochester

Chang, Chawnshang

<120> Non-androgen Dependent Roles for
Androgen Receptor and Non-androgen Related Inhibitors of
Androgen Receptor

<130> 21108.0037P1

<140> Unassigned

<141> 2004-12-13

<150> 60/529,011

<151> 2003-12-12

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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Ala	Ile	Ser	Ala	Val	Val	Asp	Asn	Tyr	Ile	Arg	Ser	Arg	Arg	Asp	Ile	20	25	30	
Arg	Ser	Leu	Pro	Glu	Asn	Ile	Gln	Phe	Asp	Val	Tyr	Tyr	Lys	Leu	Tyr	35	40	45	
Gln	Gln	Gly	Arg	Leu	Cys	Gln	Leu	Gly	Ser	Glu	Phe	Cys	Glu	Leu	Glu	50	55	60	
Val	Phe	Ala	Lys	Val	Leu	Arg	Ala	Leu	Asp	Lys	Arg	His	Leu	Leu	His	65	70	75	80
His	Cys	Phe	Gln	Ala	Leu	Met	Asp	His	Gly	Val	Lys	Val	Ala	Ser	Val	85	90	95	
Leu	Ala	Tyr	Ser	Phe	Ser	Arg	Arg	Cys	Ser	Tyr	Ile	Ala	Glu	Ser	Asp	100	105	110	
Ala	Ala	Val	Lys	Glu	Lys	Ala	Ile	Gln	Val	Gly	Phe	Val	Leu	Gly	Gly	115	120	125	
Phe	Leu	Ser	Asp	Ala	Gly	Trp	Tyr	Ser	Asp	Ala	Glu	Lys	Val	Phe	Leu	130	135	140	
Ser	Cys	Leu	Gln	Leu	Cys	Thr	Leu	His	Asp	Glu	Met	Leu	His	Trp	Phe	145	150	155	160
Arg	Ala	Val	Glu	Cys	Cys	Val	Arg	Leu	Leu	His	Val	Arg	Asn	Gly	Asn	165	170	175	
Cys	Lys	Tyr	His	Leu	Gly	Glu	Glu	Thr	Phe	Lys	Leu	Ala	Gln	Thr	Tyr	180	185	190	
Met	Asp	Lys	Leu	Ser	Lys	His	Gly	Gln	Gln	Ala	Asn	Lys	Ala	Ala	Leu	195	200	205	
Tyr	Gly	Glu	Leu	Cys	Ala	Leu	Leu	Phe	Ala	Lys	Ser	His	Tyr	Asp	Glu	210	215	220	

Ala	Tyr	Lys	Trp	Cys	Ile	Glu	Ala	Met	Lys	Glu	Ile	Thr	Ala	Gly	Leu	
225					230					235					240	
Pro	Val	Lys	Val	Val	Val	Asp	Val	Leu	Arg	Gln	Ala	Ser	Lys	Ala	Cys	
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Val	Val	Lys	Arg	Glu	Phe	Lys	Lys	Ala	Glu	Gln	Leu	Ile	Lys	His	Ala	
			260					265					270			
Val	Tyr	Leu	Ala	Arg	Asp	His	Phe	Gly	Ser	Lys	His	Pro	Lys	Tyr	Ser	
	275						280					285				
Asp	Thr	Leu	Leu	Asp	Tyr	Gly	Phe	Tyr	Leu	Leu	Asn	Val	Asp	Asn	Ile	
	290					295					300					
Cys	Gln	Ser	Val	Ala	Ile	Tyr	Gln	Ala	Ala	Leu	Asp	Ile	Arg	Gln	Ser	
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Val	Phe	Gly	Gly	Lys	Asn	Ile	His	Val	Ala	Thr	Ala	His	Glu	Asp	Leu	
			325					330						335		
Ala	Tyr	Ser	Ser	Tyr	Val	His	Gln	Tyr	Ser	Ser	Gly	Lys	Phe	Asp	Asn	
			340					345					350			
Ala	Leu	Phe	His	Ala	Glu	Arg	Ala	Ile	Gly	Ile	Ile	Thr	His	Ile	Leu	
	355						360					365				
Pro	Glu	Asp	His	Leu	Leu	Leu	Ala	Ser	Ser	Lys	Arg	Val	Lys	Ala	Leu	
	370					375					380					
Ile	Leu	Glu	Glu	Ile	Ala	Ile	Asp	Cys	His	Asn	Lys	Glu	Thr	Glu	Gln	
385					390					395					400	
Arg	Leu	Leu	Gln	Glu	Ala	His	Asp	Leu	His	Leu	Ser	Ser	Leu	Gln	Leu	
			405					410						415		
Ala	Lys	Lys	Ala	Phe	Gly	Glu	Phe	Asn	Val	Gln	Thr	Ala	Lys	His	Tyr	
			420					425					430			
Gly	Asn	Leu	Gly	Arg	Leu	Tyr	Gln	Ser	Met	Arg	Lys	Phe	Lys	Glu	Ala	
	435						440					445				
Glu	Glu	Met	His	Ile	Lys	Ala	Ile	Gln	Ile	Lys	Glu	Gln	Leu	Leu	Gly	
	450					455					460					
Gln	Glu	Asp	Tyr	Glu	Val	Ala	Leu	Ser	Val	Gly	His	Leu	Ala	Ser	Leu	
465					470					475					480	
Tyr	Asn	Tyr	Asp	Met	Asn	Gln	Tyr	Glu	Asn	Ala	Glu	Lys	Leu	Tyr	Leu	
			485					490						495		
Arg	Ser	Ile	Ala	Ile	Gly	Lys	Lys	Leu	Phe	Gly	Glu	Gly	Tyr	Ser	Gly	
			500					505					510			
Leu	Glu	Tyr	Asp	Tyr	Arg	Gly	Leu	Ile	Lys	Leu	Tyr	Asn	Ser	Ile	Gly	
	515						520					525				
Asn	Tyr	Glu	Lys	Val	Phe	Glu	Tyr	His	Asn	Val	Leu	Ser	Asn	Trp	Asn	
	530					535					540					
Arg	Leu	Arg	Asp	Arg	Gln	Tyr	Ser	Val	Thr	Asp	Ala	Leu	Glu	Asp	Val	
545					550					555					560	
Ser	Thr	Ser	Pro	Gln	Ser	Thr	Glu	Glu	Val	Val	Gln	Ser	Phe	Leu	Ile	
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<210> 2

<211> 1758

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

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tttgatgttt	actacaagct	ttaccaacag	ggacgcttat	gtcaactggg	cagtgaattt	180
tgtgaattgg	aagtttttgc	taaagtactg	agagcttttg	ataaaagaca	tttgcttcat	240

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cagggtggct ttgttttagg tggctttctt tcagatgcag gctgggtacag tgatgctgag 420
aaagtttttc tgtcctgcct tcagtttgtg actctacacg atgagatgct tcattgggttt 480
cgtgcagtag aatgttttgt gaggttgctt catgtgcgaa atggaaactg caaatatcat 540
ttgggtgaag aaacatttaa attagctcag acatatatgg ataaactatc aaaacatggc 600
cagcaagcaa ataaagctgc actctatgga gaactgtgtg cactcctatt tgcaaaaagt 660
cactatgatg aggcatacaa atgggtgcac gaggcaatga aagaaattac agcaggctta 720
ccagtgaag ttgtgggtgga tgtcttaaga caagcttcta aggcttggtg agtaaaacgt 780
gaatttaaga aggcagaaca gttaattaaa catgcagtgt atttggcacg ggatcatttt 840
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tttggggaat ttaatgtaca gactgcaaaa cactatggaa accttggaag actttatcag 1320
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caacttcttg gtcaagaaga ttatgaagta gccctttcag tgggacatct ggcttcttta 1440
tataattatg acatgaatca gtatgaaaat gctgagaaac tttatttgcg atctatagca 1500
attgggaaga aacttttttg tgagggctac agtggactag aatatgatta tcgagggtctc 1560
attaaacttt acaactccat tggaaattac gagaaagtgt ttgaatatca caatgttctg 1620
tctaactgga accggttgcg agatcggcaa tattcagtga cagatgctct tgaagatgtc 1680
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<210> 3

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3

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 20           25           30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35           40           45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
 50           55           60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
 65           70           75           80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
 85           90           95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
100           105           110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
115           120           125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
130           135           140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
145           150           155           160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
165           170           175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
180           185           190

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Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser
				245					250					255	
Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met	Tyr	Ala	Pro	Leu	Leu	Gly
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Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Ala	Glu	Cys
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Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly	Lys	Ser	Thr	Glu	Asp	Thr
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Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu	Glu	Gly
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Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser	Gly	Thr
				325					330					335	
Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp
			340					345					350		
Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala
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Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Pro	His	Ala	Arg
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Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala
385					390					395					400
Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Ala	Gly
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Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser	Ser	Ser
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Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Cys
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Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	450					455					460				
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465					470					475					480
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Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val	Pro
			500					505					510		
Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Asp
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Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg	Asp
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His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu
545					550					555					560
Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys
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Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys
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Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg
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Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln
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Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile
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Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
 675 680 685
 His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
 690 695 700
 Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
 705 710 715 720
 Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
 725 730 735
 Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
 740 745 750
 Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
 755 760 765
 Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
 770 775 780
 Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
 785 790 795 800
 Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile
 805 810 815
 Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
 820 825 830
 Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
 835 840 845
 Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
 850 855 860
 Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
 865 870 875 880
 Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
 885 890 895
 Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys
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 Pro Ile Tyr Phe His Thr Gln
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<210> 4

<211> 4321

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 4

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cacatcctgc	tcaagacgct	tctaccagct	caccaagctc	ctggactccg	tgcagcctat	3720
tgcgagagag	ctgcatcagt	tcacttttga	cctgctaate	aagtcacaca	tgggtgagcgt	3780
ggactttccg	gaaatgatgg	cagagatcat	ctctgtgcaa	gtgcccaga	tcctttctgg	3840
gaaagtcaag	cccatctatt	tccacaccca	gtgaagcatt	ggaaacccta	tttccccacc	3900
ccagctcatg	ccccctttca	gatgtcttct	gcctgttata	actctgcact	actcctctgc	3960
agtgccttgg	ggaatttcct	ctattgatgt	acagtctgtc	atgaacatgt	tcctgaattc	4020
tatttgctgg	gctttttttt	tctctttctc	tcctttcttt	ttctttcttc	ctccctatct	4080
aaccctccca	tggcaccttc	agactttgct	tcccatgtgt	gctcctatct	gtgtttttgaa	4140
tgggtgttga	tgccttttaa	tctgtgatga	tcctcatatg	gcccagtgtc	aagttgtgct	4200
tgtttacagc	actactctgt	gccagccaca	caaacgttta	cttatcttat	gccacgggaa	4260
gttttagagag	ctaagattat	ctgggggaaat	caaaacaaaa	aacaagcaaa	caaaaaaaaaa	4320
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<210> 5

<211> 433

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5

Met	Ser	Gly	Arg	Pro	Arg	Thr	Thr	Ser	Phe	Ala	Glu	Ser	Cys	Lys	Pro
1				5				10					15		
Val	Gln	Gln	Pro	Ser	Ala	Phe	Gly	Ser	Met	Lys	Val	Ser	Arg	Asp	Lys
			20					25					30		
Asp	Gly	Ser	Lys	Val	Thr	Thr	Val	Val	Ala	Thr	Pro	Gly	Gln	Gly	Pro
		35					40					45			
Asp	Arg	Pro	Gln	Glu	Val	Ser	Tyr	Thr	Asp	Thr	Lys	Val	Ile	Gly	Asn
	50					55					60				
Gly	Ser	Phe	Gly	Val	Val	Tyr	Gln	Ala	Lys	Leu	Cys	Asp	Ser	Gly	Glu
65				70				75							80
Leu	Val	Ala	Ile	Lys	Lys	Val	Leu	Gln	Asp	Lys	Arg	Phe	Lys	Asn	Arg
			85					90						95	
Glu	Leu	Gln	Ile	Met	Arg	Lys	Leu	Asp	His	Cys	Asn	Ile	Val	Arg	Leu
			100					105					110		
Arg	Tyr	Phe	Phe	Tyr	Ser	Ser	Gly	Glu	Lys	Lys	Asp	Glu	Val	Tyr	Leu
		115					120					125			
Asn	Leu	Val	Leu	Asp	Tyr	Val	Pro	Glu	Thr	Val	Tyr	Arg	Val	Ala	Arg
	130					135					140				
His	Tyr	Ser	Arg	Ala	Lys	Gln	Thr	Leu	Pro	Val	Ile	Tyr	Val	Lys	Leu
145				150						155					160
Tyr	Met	Tyr	Gln	Leu	Phe	Arg	Ser	Leu	Ala	Tyr	Ile	His	Ser	Phe	Gly
			165					170						175	
Ile	Cys	His	Arg	Asp	Ile	Lys	Pro	Gln	Asn	Leu	Leu	Leu	Asp	Pro	Asp
			180					185					190		
Thr	Ala	Val	Leu	Lys	Leu	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val
		195					200					205			
Arg	Gly	Glu	Pro	Asn	Val	Ser	Tyr	Ile	Cys	Ser	Arg	Tyr	Tyr	Arg	Ala
	210					215					220				
Pro	Glu	Leu	Ile	Phe	Gly	Ala	Thr	Asp	Tyr	Thr	Ser	Ser	Ile	Asp	Val
225				230						235					240
Trp	Ser	Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Ile
			245					250						255	
Phe	Pro	Gly	Asp	Ser	Gly	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val
		260					265						270		
Leu	Gly	Thr	Pro	Thr	Arg	Glu	Gln	Ile	Arg	Glu	Met	Asn	Pro	Asn	Tyr
		275					280					285			
Thr	Glu	Phe	Lys	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	Thr	Lys	Asp
	290					295					300				
Ser	Ser	Gly	Thr	Gly	His	Phe	Thr	Ser	Gly	Val	Arg	Val	Phe	Arg	Pro
305					310					315					320
Arg	Thr	Pro	Pro	Glu	Ala	Ile	Ala	Leu	Cys	Ser	Arg	Leu	Leu	Glu	Tyr
			325					330						335	
Thr	Pro	Thr	Ala	Arg	Leu	Thr	Pro	Leu	Glu	Ala	Cys	Ala	His	Ser	Phe
			340					345					350		
Phe	Asp	Glu	Leu	Arg	Asp	Pro	Asn	Val	Lys	Leu	Pro	Asn	Gly	Arg	Asp
		355					360					365			
Thr	Pro	Ala	Leu	Phe	Asn	Phe	Thr	Thr	Gln	Glu	Leu	Ser	Ser	Asn	Pro
	370					375					380				
Pro	Leu	Ala	Thr	Ile	Leu	Ile	Pro	Pro	His	Ala	Arg	Ile	Gln	Ala	Ala
385				390						395					400
Ala	Ser	Thr	Pro	Thr	Asn	Ala	Thr	Ala	Ala	Ser	Asp	Ala	Asn	Thr	Gly
			405					410						415	
Asp	Arg	Gly	Gln	Thr	Asn	Asn	Ala	Ala	Ser	Ala	Ser	Ala	Ser	Asn	Ser
			420				425						430		
Thr															

<210> 6
 <211> 1639
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 6
 atcatctata tgttaaataat ccgtgccgat ctgtcttgaa ggagaaatat atcgcttggt 60
 ttgtttttta tagtatacaa aaggagttaa aagccaagag gacgaagtct ttttcttttt 120
 cttctgtggg agaacttaat gctgcattta tcgttaacct aacaccccaa cataaagaca 180
 aaaggaagaa aaggaggaag gaaggaaaag gtgattcgcg aagagagtga tcatgtcagg 240
 gcggcccaga accacctcct ttgcgggagag ctgcaagccg gtgcagcagc cttcagcttt 300
 tggcagcatg aaagttagca gagacaagga cggcagcaag gtgacaacag tgggtggcaac 360
 tcctgggagc ggtccagaca ggccacaaga agtcagctat acagacacta aagtgattgg 420
 aaatggatca tttgggtgtg tatatcaagc caaactttgt gattcaggag aactggtcgc 480
 catcaagaaa gtattgcagg acaagagatt taagaatcga gagctccaga tcatgagaaa 540
 gctagatcac tgtaacatag tccgattgag ttatttcttc tactccagtg gtgagaagaa 600
 agatgaggtc tatcttaatc tgggtgctgga ctatgttccg gaaacagtat acagagttgc 660
 cagacactat agtcgagcca aacagacgct ccctgtgatt tatgtcaagt tgtatatgta 720
 tcagctgttc cgaagtttag cctatatcca ttcctttgga atctgccatc gggatattaa 780
 accgcagaac ctcttggttg atcctgatac tgctgtatta aaactctgtg actttggaag 840
 tgcaaagcag ctggtccgag gagaacccaa tgtttcgtat atctgttctc ggtactatag 900
 ggcaccagag ttgatctttg gagccactga ttataacctc agtatagatg tatgggtctgc 960
 tggctgtgtg ttggctgagc tgttactagg acaaccaata tttccagggg atagtgggtg 1020
 ggatcagttg gtagaaataa tcaaggctct gggaactcca acaaggggagc aaatcagaga 1080
 aatgaacca aactacacag aattttaaatt ccctcaaatt aaggcacatc cttggactaa 1140
 ggattcgtca ggaacaggac atttcacctc aggagtgcgg gtcttccgac cccgaactcc 1200
 accggaggca attgcactgt gtagccgtct gctggagtat acaccaactg cccgactaac 1260
 accactggaa gcttgtgcac attcattttt tgatgaatta cgggacccaa atgtcaaact 1320
 accaaatggg cgagacacac ctgcactctt caacttcacc actcaagaac tgtcaagtaa 1380
 tccacctctg gctaccatcc ttattcctcc tcatgctcgg attcaagcag ctgcttcaac 1440
 cccacaaat gccacagcag cgtcagatgc taatactgga gaccgtggac agaccaataa 1500
 tgctgcttct gcatcagctt ccaactccac ctgaacagtc ccgagcagcc agctgcacag 1560
 gaaaaaccac cagttacttg agtgtcactc agcaacactg gtcacgtttg gaaagaatat 1620
 taaaaaaaaa aaaaaaaaaa 1639

<210> 7
 <211> 391
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 7
 Met Lys Cys Leu Val Thr Gly Gly Asn Val Lys Val Leu Gly Lys Ala
 1 5 10 15
 Val His Ser Leu Ser Arg Ile Gly Asp Glu Leu Tyr Leu Glu Pro Leu
 20 25 30
 Glu Asp Gly Leu Ser Leu Arg Thr Val Asn Ser Ser Arg Ser Ala Tyr
 35 40 45
 Ala Cys Phe Leu Phe Ala Pro Leu Phe Phe Gln Gln Tyr Gln Ala Ala
 50 55 60
 Thr Pro Gly Gln Asp Leu Leu Arg Cys Lys Ile Leu Met Lys Ser Phe
 65 70 75 80

Leu Ser Val Phe Arg Ser Leu Ala Met Leu Glu Lys Thr Val Glu Lys
 85 90 95
 Cys Cys Ile Ser Leu Asn Gly Arg Ser Ser Arg Leu Val Val Gln Leu
 100 105 110
 His Cys Lys Phe Gly Val Arg Lys Thr His Asn Leu Ser Phe Gln Asp
 115 120 125
 Cys Glu Ser Leu Gln Ala Val Phe Asp Pro Ala Ser Cys Pro His Met
 130 135 140
 Leu Arg Ala Pro Ala Arg Val Leu Gly Glu Ala Val Leu Pro Phe Ser
 145 150 155 160
 Pro Ala Leu Ala Glu Val Thr Leu Gly Ile Gly Arg Gly Arg Arg Val
 165 170 175
 Ile Leu Arg Ser Tyr His Glu Glu Glu Ala Asp Ser Thr Ala Lys Ala
 180 185 190
 Met Val Thr Glu Met Cys Leu Gly Glu Glu Asp Phe Gln Gln Leu Gln
 195 200 205
 Ala Gln Glu Gly Val Ala Ile Thr Phe Cys Leu Lys Glu Phe Arg Gly
 210 215 220
 Leu Leu Ser Phe Ala Glu Ser Ala Asn Leu Asn Leu Ser Ile His Phe
 225 230 235 240
 Asp Ala Pro Gly Arg Pro Ala Ile Phe Thr Ile Lys Asp Ser Leu Leu
 245 250 255
 Asp Gly His Phe Val Leu Ala Thr Leu Ser Asp Thr Asp Ser His Ser
 260 265 270
 Gln Asp Leu Gly Ser Pro Glu Arg His Gln Pro Val Pro Gln Leu Gln
 275 280 285
 Ala His Ser Thr Pro His Pro Asp Asp Phe Ala Asn Asp Asp Ile Asp
 290 295 300
 Ser Tyr Met Ile Ala Met Glu Thr Thr Ile Gly Asn Glu Gly Ser Arg
 305 310 315 320
 Val Leu Pro Ser Ile Ser Leu Ser Pro Gly Pro Gln Pro Pro Lys Ser
 325 330 335
 Pro Gly Pro His Ser Glu Glu Glu Asp Glu Ala Glu Pro Ser Thr Val
 340 345 350
 Pro Gly Thr Pro Pro Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser
 355 360 365
 Ile Leu Ala Pro Val Arg Ser Pro Gln Gly Pro Ser Pro Val Leu Ala
 370 375 380
 Glu Asp Ser Glu Gly Glu Gly
 385 390

<210> 8

<211> 2102

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 syntnetic construct

<400> 8

gcgcgggaag	ggaccccgga	cccggagggtc	gcggagagct	gggcagtgtt	ggccgctggc	60
ggagcgctgg	ggcagcatga	agtgcctggt	cacgggcggc	aacgtgaagg	tgctcggcaa	120
ggccgtccac	tccctgtccc	gcacgcggga	cgagctctac	ctggaaccct	tggaggacgg	180
gctctccctc	cggacggtga	actcctcccg	ctctgcctat	gcctgctttc	tctttgcccc	240
gctcttcttc	cagcaatacc	aggcagccac	ccctgggtcag	gacctgctgc	gctgtaagat	300
cctgatgaag	tctttcctgt	ctgtcttccg	ctcactggcg	atgctggaga	agacggtgga	360
aaaatgctgc	atctccctga	atggccggag	cagccgcctg	gtgggtccagc	tgcattgcaa	420
gttcgggggtg	cgaagactc	acaacctgtc	cttccaggac	tgtgagtgcc	tgcaggccgt	480
cttcgaccca	gcctcgtgcc	cccacatgct	ccgcgccccca	gcacgggttc	tgggggagggc	540
tggtctgccc	ttctctcctg	cactgggtga	agtgacgctg	ggcattggcc	gtggccgcag	600

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ggtcattcctg cgcagctacc acgaggagga ggcagacagc actgccaaag ccatgggtgac 660
tgagatgtgc cttggagagg aggatttcca gcagctgcag gccaggaag ggggtggccat 720
cactttctgc ctcaaggaat tccgggggct cctgagcttt gcagagtcag caaacttgaa 780
tcttagcatt cattttgatg ctccaggcag gcccgccatc ttcaccatca aggactcttt 840
gctggacggc cactttgtct tggccacact ctccagacacc gactcgcact cccaggacct 900
gggctcccca gagcgtcacc agccagtgcc tcagctccag gctcacagca caccaccacc 960
ggacgacttt gccaatgacg acattgactc ttacatgata gccatggaaa ccactatagg 1020
caatgagggc tcgcgggtgc tgccctccat ttccctttca cctggccccc agccccccaa 1080
gagccccggt cccactccg aggaggaaga tgaggctgag ccagtagacag tgccctgggac 1140
tccccaccac aagaagtcc gctcactgtt cttcggctcc atcctggccc ctgtacgctc 1200
ccccagggc cccagccctg tgctggcgga agacagttag ggtgaaggct gaaccaagaa 1260
cctgaagcct gtaccagag gccttggaact agacgaagcc ccagccagtg gcagaactgg 1320
gtctctcagc cctggggatc agaaagggtg gcttgctgga gctgagctgt ttcactgcct 1380
ctcgcaggcc ccagctggct gtcactgtaa agctgtccca cagcggtcgg gcctgggccc 1440
ttatctcccc acaaccccca gccaatcagg actttccaga cttggccctg aactactgac 1500
gttcctacct cttattttctc attgagcctc aggctatact ccagctggcc aaggctggaa 1560
acctgtctcc ctccaggtca ccttcctaag gaaaatgtca tagtaggtgc tgctggcccc 1620
tggtgatcca gcttctctgc caatcatgac ctgttccttc ctgaagtcct gggcatgcat 1680
ctgggacccc cgtggagctg acaagtttcc cttgctttcc tgatactctt tggcgctgac 1740
ttggaattct aagagccttg gacccgagtg tgtggctagg gttgccctgg ctggggcccg 1800
gtgccgagac tcccaagcgg ctctgtgcag aagagctgcc aggcagtgtc ttagatgtga 1860
gacggaggcc atggcgagaa tccagctttg acctttattc aagagaccag atgggttgcc 1920
ccaggatccg gctgccagcc ctgaggccaa gcacggctgg agaccacga cctggcctgc 1980
cgttgccctg agctgcagcc tcggccccag gatcctgctc acagtcaccg caggtgcagg 2040
caggaagcag ccctggggga ctggacgctg ctattgattc attaaaaaa gaaaagaaaa 2100
at 2102

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<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9

gggcccctgg atggatagct ac

22

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10

gtagctatcc atccaggggc c

21

<210> 11

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

gggcccttg atggatagct acctcgaggt agctatccat ccaggggcc

49

<210> 12

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

tttttgggcc cctggatgga tagctacctc gaggtagcta tccatccagg ggcc

54

<210> 13

<211> 483

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 13

Met	Ala	Thr	Ile	Glu	Glu	Ile	Ala	His	Gln	Ile	Ile	Glu	Gln	Gln	Met	1	5	10	15
Gly	Glu	Ile	Val	Thr	Glu	Gln	Gln	Thr	Gly	Gln	Lys	Ile	Gln	Ile	Val	20	25	30	
Thr	Ala	Leu	Asp	His	Asn	Thr	Gln	Gly	Lys	Gln	Phe	Ile	Leu	Thr	Asn	35	40	45	
His	Asp	Gly	Ser	Thr	Pro	Ser	Lys	Val	Ile	Leu	Ala	Arg	Gln	Asp	Ser	50	55	60	
Thr	Pro	Gly	Lys	Val	Phe	Leu	Thr	Thr	Pro	Asp	Ala	Ala	Gly	Val	Asn	65	70	75	80
Gln	Leu	Phe	Phe	Thr	Thr	Pro	Asp	Leu	Ser	Ala	Gln	His	Leu	Gln	Leu	85	90	95	
Leu	Thr	Asp	Asn	Ser	Pro	Asp	Gln	Gly	Pro	Asn	Lys	Val	Phe	Asp	Leu	100	105	110	
Cys	Val	Val	Cys	Gly	Asp	Lys	Ala	Ser	Gly	Arg	His	Tyr	Gly	Ala	Val	115	120	125	
Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Lys	Arg	Ser	Ile	Arg	Lys	Asn	130	135	140	
Leu	Val	Tyr	Ser	Cys	Arg	Gly	Ser	Lys	Asp	Cys	Ile	Ile	Asn	Lys	His	145	150	155	160
His	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Leu	Gln	Arg	Cys	Ile	Ala	Phe	165	170	175	
Gly	Met	Lys	Gln	Asp	Ser	Val	Gln	Cys	Glu	Arg	Lys	Pro	Ile	Glu	Val	180	185	190	
Ser	Arg	Glu	Lys	Ser	Ser	Asn	Cys	Ala	Ala	Ser	Thr	Glu	Lys	Ile	Tyr	195	200	205	
Ile	Arg	Lys	Asp	Leu	Arg	Ser	Pro	Leu	Thr	Ala	Thr	Pro	Thr	Phe	Val	210	215	220	
Thr	Asp	Ser	Glu	Ser	Thr	Arg	Ser	Thr	Gly	Leu	Leu	Asp	Ser	Gly	Met	225	230	235	240
Phe	Met	Asn	Ile	His	Pro	Ser	Gly	Val	Lys	Thr	Glu	Ser	Ala	Val	Leu	245	250	255	
Met	Thr	Ser	Asp	Lys	Ala	Glu	Ser	Cys	Gln	Gly	Asp	Leu	Ser	Thr	Leu	260	265	270	
Ala	Asn	Val	Val	Thr	Ser	Leu	Ala	Asn	Leu	Gly	Lys	Thr	Lys	Asp	Leu	275	280	285	

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Ser Gln Asn Ser Asn Glu Met Ser Met Ile Glu Ser Leu Ser Asn Asp
 290                295                300
Asp Thr Ser Leu Cys Glu Phe Gln Glu Met Gln Thr Asn Gly Asp Val
305                310                315                320
Ser Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu Asn Pro Gly Glu Ser
                325                330                335
Thr Ala Cys Gln Ser Ser Val Ala Gly Met Glu Gly Ser Val His Leu
                340                345                350
Ile Thr Gly Asp Ser Ser Ile Asn Tyr Thr Glu Lys Glu Gly Pro Leu
                355                360                365
Leu Ser Asp Ser His Val Ala Phe Arg Leu Thr Met Pro Ser Pro Met
                370                375                380
Pro Glu Tyr Leu Asn Val His Tyr Ile Gly Glu Ser Ala Ser Arg Leu
385                390                395                400
Leu Phe Leu Ser Met His Trp Ala Leu Ser Ile Pro Ser Phe Gln Ala
                405                410                415
Leu Gly Gln Glu Asn Ser Ile Ser Leu Val Lys Ala Tyr Trp Asn Glu
                420                425                430
Leu Phe Thr Leu Gly Leu Ala Gln Cys Trp Gln Val Met Asn Val Ala
                435                440                445
Thr Ile Leu Ala Thr Phe Val Asn Cys Leu His Asn Ser Leu Gln Gln
                450                455                460
Asp Ala Lys Val Ile Ala Ala Leu Ile His Phe Thr Arg Arg Ala Ile
465                470                475                480
Thr Asp Leu

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<210> 14

<211> 596

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

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Met Thr Ser Pro Ser Pro Arg Ile Gln Ile Ile Ser Thr Asp Ser Ala
 1                5                10                15
Val Ala Ser Pro Gln Arg Ile Gln Ile Val Thr Asp Gln Gln Thr Gly
                20                25                30
Gln Lys Ile Gln Ile Val Thr Ala Val Asp Ala Ser Gly Ser Pro Lys
                35                40                45
Gln Gln Phe Ile Leu Thr Ser Pro Asp Gly Ala Gly Thr Gly Lys Val
                50                55                60
Ile Leu Ala Ser Pro Glu Thr Ser Ser Ala Lys Gln Leu Ile Phe Thr
65                70                75                80
Thr Ser Asp Asn Leu Val Pro Gly Arg Ile Gln Ile Val Thr Asp Ser
                85                90                95
Ala Ser Val Glu Arg Leu Leu Gly Lys Thr Asp Val Gln Arg Pro Gln
                100                105                110
Val Val Glu Tyr Cys Val Val Cys Gly Asp Lys Ala Ser Gly Arg His
                115                120                125
Tyr Gly Ala Val Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser
                130                135                140
Val Arg Lys Asn Leu Thr Tyr Ser Cys Arg Ser Asn Gln Asp Cys Ile
145                150                155                160
Ile Asn Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Lys Lys
                165                170                175
Cys Leu Glu Met Gly Met Lys Met Glu Ser Val Gln Ser Glu Arg Lys
                180                185                190

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Pro Phe Asp Val Gln Arg Glu Lys Pro Ser Asn Cys Ala Ala Ser Thr
    195                200                205
Glu Lys Ile Tyr Ile Arg Lys Asp Leu Arg Ser Pro Leu Ile Ala Thr
    210                215                220
Pro Thr Phe Val Ala Asp Lys Asp Gly Ala Arg Gln Thr Gly Leu Leu
    225                230                235                240
Asp Pro Gly Met Leu Val Asn Ile Gln Gln Pro Leu Ile Arg Glu Asp
    245                250                255
Gly Thr Val Leu Leu Ala Thr Asp Ser Lys Ala Glu Thr Ser Gln Gly
    260                265                270
Ala Leu Gly Thr Leu Ala Asn Val Val Thr Ser Leu Ala Asn Leu Ser
    275                280                285
Glu Ser Leu Asn Asn Gly Asp Thr Ser Glu Ile Gln Pro Glu Asp Gln
    290                295                300
Ser Ala Ser Glu Ile Thr Arg Ala Phe Asp Thr Leu Ala Lys Ala Leu
    305                310                315                320
Asn Thr Thr Asp Ser Ser Ser Ser Pro Ser Leu Ala Asp Gly Ile Asp
    325                330                335
Thr Ser Gly Gly Gly Ser Ile His Val Ile Ser Arg Asp Gln Ser Thr
    340                345                350
Pro Ile Ile Glu Val Glu Gly Pro Leu Leu Ser Asp Thr His Val Thr
    355                360                365
Phe Lys Leu Thr Met Pro Ser Pro Met Pro Glu Tyr Leu Asn Val His
    370                375                380
Tyr Ile Cys Glu Ser Ala Ser Arg Leu Leu Phe Leu Ser Met His Trp
    385                390                395                400
Ala Arg Ser Ile Pro Ala Phe Gln Ala Leu Gly Gln Asp Cys Asn Thr
    405                410                415
Ser Leu Val Arg Ala Cys Trp Asn Glu Leu Phe Thr Leu Gly Leu Ala
    420                425                430
Gln Cys Ala Gln Val Met Ser Leu Ser Thr Ile Leu Ala Ala Ile Val
    435                440                445
Asn His Leu Gln Asn Ser Ile Gln Glu Asp Lys Leu Ser Gly Asp Arg
    450                455                460
Ile Lys Gln Val Met Glu His Ile Trp Lys Leu Gln Glu Phe Cys Asn
    465                470                475                480
Ser Met Ala Lys Leu Asp Ile Asp Gly Tyr Glu Tyr Ala Tyr Leu Lys
    485                490                495
Ala Ile Val Leu Phe Ser Pro Asp His Pro Gly Leu Thr Ser Thr Ser
    500                505                510
Gln Ile Glu Lys Phe Gln Glu Lys Ala Gln Met Glu Leu Gln Asp Tyr
    515                520                525
Val Gln Lys Thr Tyr Ser Glu Asp Thr Tyr Arg Leu Ala Arg Ile Leu
    530                535                540
Val Arg Leu Pro Ala Leu Arg Leu Met Ser Ser Asn Ile Thr Glu Glu
    545                550                555                560
Leu Phe Phe Thr Gly Leu Ile Gly Asn Val Ser Ile Asp Ser Ile Ile
    565                570                575
Pro Tyr Ile Leu Lys Met Glu Thr Ala Glu Tyr Asn Gly Gln Ile Thr
    580                585                590
Gly Ala Ser Leu
    595

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<210> 15

<211> 2029

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 15

gaattcgggc	ccgtcggctt	tcttcaaccc	tctcttcccg	gagcgcccc	aatccacgag	60
tggcagccgc	gggactgtcg	cgtcggcgcc	cgacgcggag	tcagcagggg	cgaaaagcgg	120
tagatcatgg	caaccataga	agaaattgca	catcaaatta	ttgaacaaca	gatgggagag	180
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<210> 16

<211> 6450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

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23

<210> 18

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

tgctcctcc tcgtggtag

19

<210> 19

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 19
 tgccttcctt ggatgtggta g

21

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 20
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21

<210> 21
 <211> 920
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 35 40 45
 Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
 50 55 60
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser
 85 90 95
 Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu
 100 105 110
 Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu
 115 120 125
 Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly
 130 135 140
 Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala
 145 150 155 160
 Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser
 165 170 175
 Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln
 180 185 190
 Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser
 195 200 205
 Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn
 210 215 220

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Lys	Ala	Val	Ser	Val	Ser	Met	Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His
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Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met	Tyr	Ala	Pro	Leu
			260					265					270		
Leu	Gly	Val	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Ala
		275					280					285			
Glu	Cys	Lys	Gly	Ser	Leu	Leu	Asp	Asp	Ser	Ala	Gly	Lys	Ser	Thr	Glu
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Asp	Thr	Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu
305					310				315						320
Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser
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Gly	Thr	Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala
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Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly
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Ala	Gly	Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser
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Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly
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Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
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Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr
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 Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala
 725 730 735
 Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp
 740 745 750
 Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp
 755 760 765
 Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln
 770 775 780
 Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile
 785 790 795 800
 Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile
 805 810 815
 Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg
 820 825 830
 Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys
 835 840 845
 Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu
 850 855 860
 Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp
 865 870 875 880
 Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met
 885 890 895
 Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val
 900 905 910
 Lys Pro Ile Tyr Phe His Thr Gln
 915 920

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 Pro Lys Lys Phe Arg Ser Leu Phe Phe Gly Ser Ile
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 His Pro Thr His Ser Ser Arg Leu Trp Glu Leu Leu Met Glu Ala Thr
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 Pro Thr Met